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EXAMINER	
CHAKRABARTI,A	
ART UNIT	**PAPER NUMBER**
1655	8

DATE MAILED: 11/08/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Office Action Summary

Application No.	Applicant(s)
09/381,480	Chee
Examiner	**Group Art Unit**
Arun Chakrabarti	1655

☒ *Responsive to communication(s) filed on* Oct 23, 2000 .

☒ *This action is* **FINAL**.

☐ *Since this application is in condition for allowance except for formal matters,* **prosecution as to the merits is closed** *in accordance with the practice under Ex parte Quayle, 1935 C.D. 11; 453 O.G. 213.*

A shortened statutory period for response to this action is set to expire 3 *month(s), or thirty days, whichever is longer, from the mailing date of this communication. Failure to respond within the period for response will cause the application to become abandoned. (35 U.S.C. § 133). Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).*

Disposition of Claims

☒ *Claim(s)* 1-15 *is/are pending in the application.*

Of the above, claim(s) _____ *is/are withdrawn from consideration.*

☐ *Claim(s)* _____ *is/are allowed.*

☒ *Claim(s)* 1-15 *is/are rejected.*

☐ *Claim(s)* _____ *is/are objected to.*

☐ *Claims* _____ *are subject to restriction or election requirement.*

Application Papers

☐ *See the attached Notice of Draftsperson's Patent Drawing Review, PTO-948.*

☐ *The drawing(s) filed on* _____ *is/are objected to by the Examiner.*

☐ *The proposed drawing correction, filed on* _____ *is* ☐*approved* ☐*disapproved.*

☐ *The specification is objected to by the Examiner.*

☐ *The oath or declaration is objected to by the Examiner.*

Priority under 35 U.S.C. § 119

☐ *Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).*

☐ *All* ☐ *Some** ☐ *None of the CERTIFIED copies of the priority documents have been*

☐ *received.*

☐ *received in Application No. (Series Code/Serial Number)* _____ .

☐ *received in this national stage application from the International Bureau (PCT Rule 17.2(a)).*

**Certified copies not received:* _____ .

☐ *Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).*

Attachment(s)

☒ *Notice of References Cited, PTO-892*

☒ *Information Disclosure Statement(s), PTO-1449, Paper No(s).* 7

☐ *Interview Summary, PTO-413*

☐ *Notice of Draftsperson's Patent Drawing Review, PTO-948*

☐ *Notice of Informal Patent Application, PTO-152*

--- SEE OFFICE ACTION ON THE FOLLOWING PAGES ---

DETAILED ACTION

Claim Rejections - 35 USC § 102

1. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless --
>
> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371© of this title before the invention thereof by the applicant for patent.

2. Claims 1-2, 5-6 and 15 are rejected under 35 U.S.C. 102 (e) as being anticipated by Cook et al. (U.S. Patent 5,698,391) (December 16, 1997).

Cook et al. teach a method of analyzing a target nucleic acid (abstract), comprising:

a)designing an array of probes comprising a probe set comprising probes complementary to a reference sequence (Example 40, Table 9 and Claim 1a);

b) hybridizing the target nucleic acid to the array of probes wherein the sequence of the target nucleic acid is a variant of the reference sequence (Example 40, Claim 1b);

c) determining the relative hybridization of the probes to the target nucleic acid (Example 40, Claim 1b);

d) estimating the sequence of the target nucleic acid from the relative hybridization of the probe (Example 40, Claim 1b and 1c);

e) providing a further array of probes comprising a probe set comprising probes complementary to the estimated sequence of the target nucleic acid (Example 40, Claim 1d);

f) hybridizing the target nucleic acid to the further array of probes (Example 40, Claim 1e);

g) determining the relative hybridization of the probes to the target nucleic acid (Example 40, Claim 1e);

h) reestimating the sequence of the target nucleic acid from the relative hybridization of the probes (Example 40, Claim 1f).

Cook et al. teach a method further comprising repeating steps (e)-(h) as necessary until the reestimated sequence of the target nucleic acid is constant between successive cycles (Example 40 and Claim 1g).

Cook et al. teach a method wherein the target nucleic acid shows 50-99% sequence identity with the reference sequence (Table 9).

Cook et al. teach a method of analyzing a target nucleic acid by designing an array of probes to be complementary to an estimated sequence of the target nucleic acid (Claim 1 and Example 40).

Claim Rejections - 35 USC § 103

3. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are

such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

4. Claims 1-2 and 5-15 are rejected under 35 U.S.C. 103 (a) over Cook et al. (U.S. Patent 5,698,391) (December 16, 1997) in view of Cronin et al. (U.S. Patent 6,027,880) (February 22, 2000)

Cook et al teach methods of claims 1-2, 5-6 and 15 as described above.

Cook et al do not teach a method wherein the reference sequence is 10 Kb nucleotides long, the array comprises a probe set comprising overlapping probes that are perfectly complementary to and span the reference sequence, and the further array comprises probes that are perfectly complementary to and span the estimated sequence.

Cronin et al. teach a method wherein the reference sequence is 10 Kb nucleotides long, the array comprises a probe set comprising overlapping probes that are perfectly complementary to and span the reference sequence, and the further array comprises probes that are perfectly complementary to and span the estimated sequence (Table 3, columns 63 and 64, Mutation Number 3849).

Cook et al do not teach a method wherein the reference sequence includes at least 90% of the human genome.

Cronin et al. teach a method wherein the reference sequence includes at least 90% of the human genome (Column 42, lines 15-25).

Cook et al do not teach a method wherein the array of probes comprises:

(1) a first probe set comprising a plurality of probes, each probe comprising a segment of at least six nucleotides exactly complementary to a subsequence of the reference sequence, the segment including at least one interrogation position complementary to a corresponding nucleotide in the reference sequence;

(2) second, third and fourth probe sets, each comprising a corresponding probe for each probe in the first probe set, the probes in the second, third and fourth probe sets being identical to a sequence comprising the corresponding probe from the first probe set or a subsequence of at least six nucleotides thereof that includes the at least one interrogation position, except that the at least one interrogation position is occupied by a different nucleotide in each of the four corresponding probes from the four probe sets.

Cronin et al. teach a method wherein the array of probes comprises:

(1) a first probe set comprising a plurality of probes, each probe comprising a segment of at least six nucleotides exactly complementary to a subsequence of the reference sequence, the segment including at least one interrogation position complementary to a corresponding nucleotide in the reference sequence (Figure 3),

(2) second, third and fourth probe sets, each comprising a corresponding probe for each probe in the first probe set, the probes in the second, third and fourth probe sets being identical to a sequence comprising the corresponding probe from the first probe set or a subsequence of at least six nucleotides thereof that includes the at least one interrogation position, except that the at

least one interrogation position is occupied by a different nucleotide in each of the four corresponding probes from the four probe sets (Figures 3, 7, 8 and 9 and Claim 28).

Cook et al do not teach a method wherein the sequence of the target nucleic acid is estimated by :

a) comparing the relative specific binding of four corresponding probes from the first, second, third and fourth probe sets ;

b) assigning a nucleotide in the sequence of the target nucleic acid as the complement of the interrogation position of the probe having the greatest specific binding ;

Cronin et al. teach a method wherein the sequence of the target nucleic acid is estimated by :

a) comparing the relative specific binding of four corresponding probes from the first, second, third and fourth probe sets (Column 164, claim 28, lines 51-53);

b) assigning a nucleotide in the sequence of the target nucleic acid as the complement of the interrogation position of the probe having the greatest specific binding (Column 164, claim 28, lines 54-56);

Cook et al do not teach a method wherein the sequence of the target nucleic acid differs from the reference by at least two positions within a probe length.

Cronin et al. teach a method wherein the sequence of the target nucleic acid differs from the reference by at least two positions within a probe length (Column 35, lines 1-6).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the sequencing of whole human genome study of Cronin et al. in the method of Cook et al., since Cronin et al. state, "The invention provides several strategies employing immobilized arrays of probes for comparing a reference sequence of known sequence with a target sequence showing substantial similarity with the reference sequence, but differing in the presence of , e.g., mutations (Column 2, lines 8-12)." An ordinary practitioner would have been motivated to combine and substitute the sequencing of whole human genome study of Cronin et al. in the method of Cook et al. in order to achieve the express advantages noted by Cronin et al. of a method which provides several strategies employing immobilized arrays of probes for comparing a reference sequence of known sequence with a target sequence showing substantial similarity with the reference sequence, but differing in the presence of , e.g., mutations.

5. Claims 1-6 and 15 are rejected under 35 U.S.C. 103 (a) over Cook et al. (U.S. Patent 5,698,391) (December 16, 1997) in view of Horwitz et al. (Journal of Virology, (1992), Vol. 66 (4), pages 2170-2179).

Cook et al teach method of claims 1, 2, 5-6 and 15 and as described above.

Cook et al do not teach method wherein the target nucleic acid sequence is a species variant of the reference sequence and wherein the reference sequence is from a human and the target nucleic acid is from a primate.

Horwitz et al teach method wherein the target nucleic acid sequence is a species variant of the reference sequence and wherein the reference sequence is from a human and the target nucleic acid is from a primate (Abstract and Figures 1 and 3).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to include the comparative primate versus human gene sequence study of Horwitz et al. in the method of Cook et al., since Horwitz et al. states "Because of the recent identification of several classes of human endogenous retroviruses and our interest in obtaining a better understanding of the evolution of human immunodeficiency virus (HIV), experiments were performed to detect the presence of HIV-1 related sequences in normal human DNA (Page 2170, column 2, second paragraph, lines 1-6)." An ordinary practitioner would have been motivated to combine the comparative primate versus human gene sequence study of Horwitz et al. in the method of Cook et al. in order to achieve the express advantages noted by Horwitz et al. of obtaining a better understanding of the evolution of human immunodeficiency virus (HIV).

Response to Amendment

6. In view of the amendment, all 112 (second paragraph) rejections are withdrawn.

Response to Arguments

7. Applicant's arguments with respect to all pending claims have been considered but are moot in view of the new ground(s) of rejection.

Conclusion

8. Applicant's submission of an information disclosure statement under 37 CFR 1.97© with the fee set forth in 37 CFR 1.17(p) on 10/23/00 prompted the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 609(B)(2)(I). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Arun Chakrabarti, Ph.D., whose telephone number is (703) 306-5818. The examiner can normally be reached on 7:00 AM-4:30 PM from Monday to Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones, can be reached on (703) 308-1152. The fax phone number for this Group is (703) 305-7401.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

W. Gary Jones
Supervisory Patent Examiner
Technology Center 1600

Arun Chakrabarti,

Patent Examiner,

November 4, 2000